CRISPR-associated sequence diversity provides new insights into evolution of *Xanthomonas albilineans*.

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Xanthomonas albilineans is the causal agent of leaf scald, a lethal disease of sugarcane

Leaf scald symptoms, including white foliar stripes and bleaching caused by albicidin that blocks chloroplast differentiation

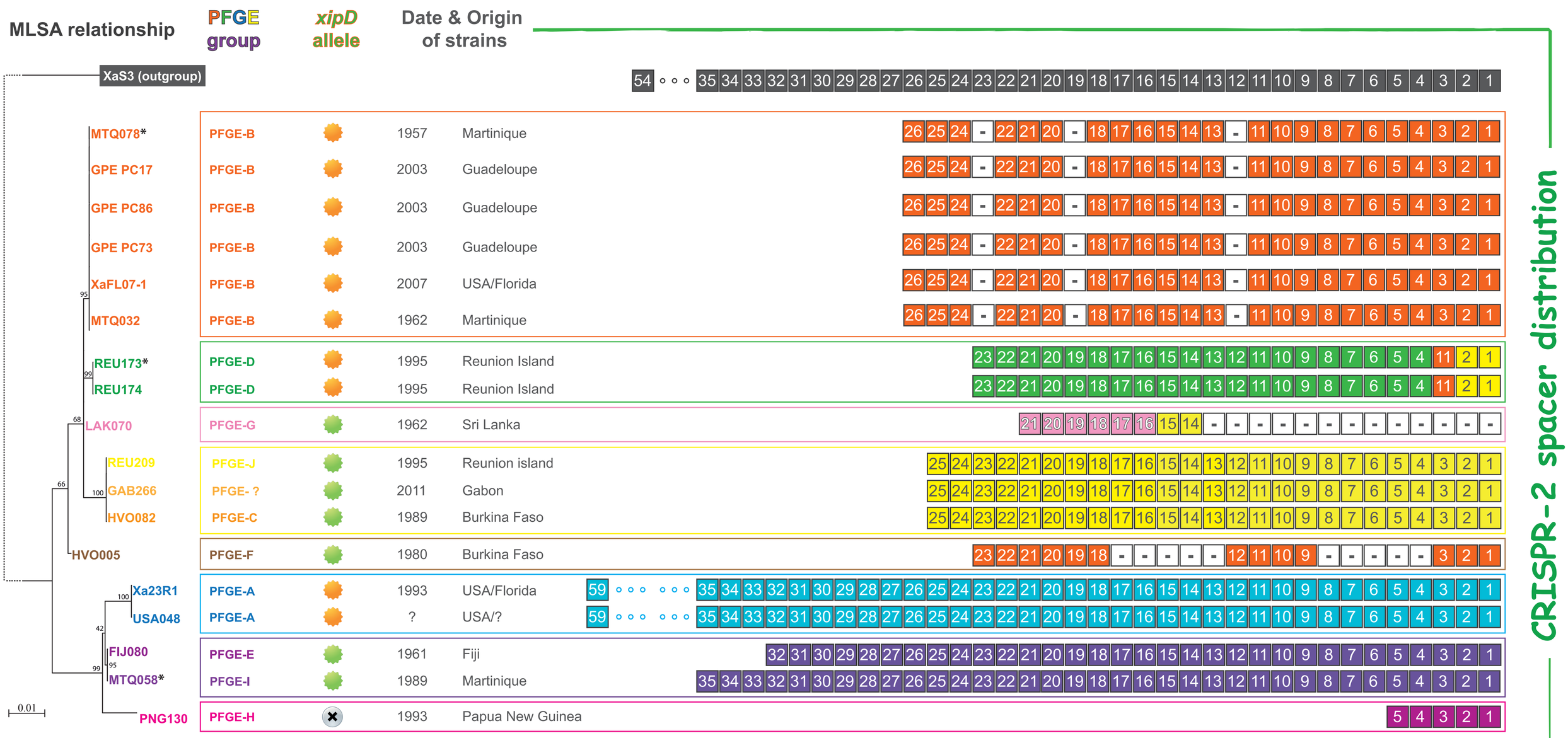
white foliar stripes | bleaching | necrosis

Xanthomonas albilineans, unlike other xanthomonads:

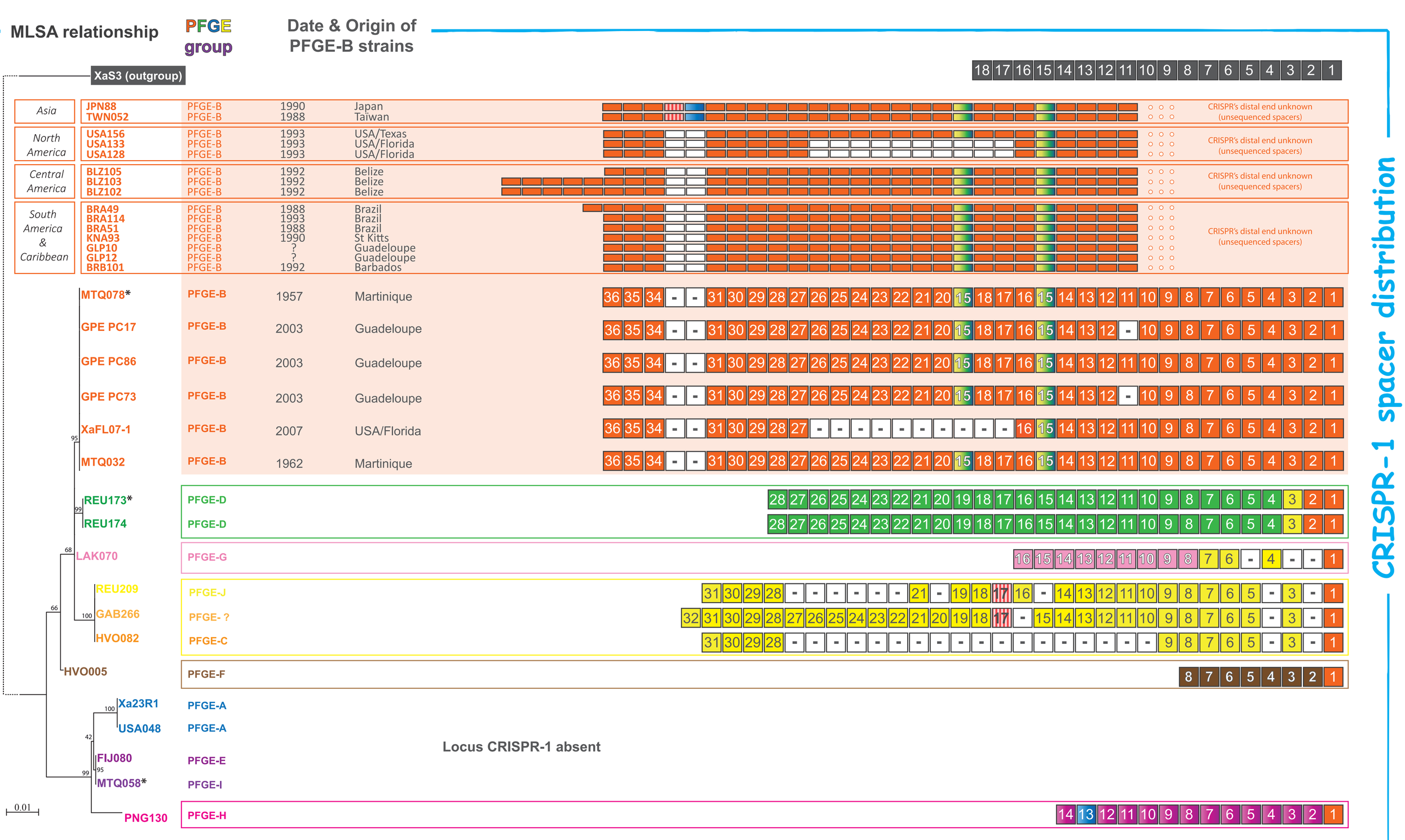
- Produces the toxin albicidin, a potent DNA gyrase inhibitor.
- Experienced a genome erosion, lacks both the gum gene cluster and the type III secretion system (T3SS) of the Hrp (Hypersensitive response and pathogenicity) injectisome families [1-2-3].
- Possesses a T3SS of the SPI-1 (*Salmonella* pathogenicity island-1) family usually found in animal pathogens [1-2-3].

Xanthomonas albilineans exhibits a large intra-species diversity, with:

- 10 genetic groups identified by Pulsed Field Gel Electrophoresis (PFGE) [4], and phylogenetic relationship between strains etablished by Multi Locus Sequence Analysis
- 2 allelic forms of the T3SS SPI-1 *xipD* gene [3].
- 2 distinct and polymorphic Clustered Regularly Interspaced Short Palindromic Repeats/cas associated genes (CRISPR/cas systems) : **CRISPR-1** and **CRISPR-2**.
  A high polymorphism of the CRISPR-spacers is observed between strains spanning the diversity of *X. albilineans.*



The CRISPR-2 spacer polymorphism allows a distribution of *X. albilineans* strains into eight distinct CRISPR-2 clades. Interestingly, this distribution is congruent with the distribution of the two allelic forms of gene *xip*D as well as with the MLSA tree, suggesting occurrence of different evolution histories of *X. albilineans.*



Within the non-ubiquitous CRISPR-1 locus, a high variability of CRISPR-spacers is observed, not only between phylogenetically distant strains but also between closely related strains. The spacers' polymorphism among strains belonging to the single PFGE-B group suggests a relationship between this variability and the geographical origin of the strains studied. It could also allow to better understand the nature of outbreaks of leaf scald disease of sugarcane that occurred in several sugarcane production regions of the world since the late 1980's.

Comments:

Strain with *: strain unsequenced (no draft available). Spacers are represented by colored and numbered squares. For each CRISPR system, squares with same color and same number are identical.

[-] : lost spacer

References:

[1] Pieretti et al. 2012. BMC Genomics, 13:658.
[2] Pieretti et al. 2009. BMC Genomics, 10:616.
[3] Marguerettaz et al. 2011. MPMI, 24:246-259.
[4] Davis et al. 1997. Phytopathology 87:316-324.